Claims

1. Method for identification of pharmaceutical targets with the following steps:

a) A plurality of gene expression patterns of similar cells is determined, with the expression rate of the gene of the cell being determined in each case;

b) The plurality of the gene expression patterns is determined such that the chronological sequence of the gene expression patterns of the cell can be at least partly reconstructed;

c) A dynamic model of the regulatory network of genome and proteome of the cell is formed by an equivalent neuronal network being formed in the following manner:

i) A gene of the genome as well as its associated protein is represented by a neuron (20) of the equivalent neuronal network;

ii) the expression rate of a gene is represented by a non-negative activity of the equivalent neuron;

iii) the regulatory effect of a protein on the gene he is represented by its synaptic connection (26) from the neuron equivalent to the protein to the neuron equivalent to the gene;

iv) the type or a regulatory effect (strengthening or inhibiting) is represented in the neuronal network by the leading sign and the strength of the associated synaptic weight (w);

d) The equivalent neuronal network is compared with the specified gene expression patterns and adapted to these;

e) From the adapted neuronal network the regulatory network of the cells investigated is deduced.

2. Method in accordance with the previous claim, characterized in that

a post-translational modification of a first protein by a second protein is represented by a synaptic connection (36) with multiplicative effect from the second neuron to the first neuron.

3. Method in accordance with one of the previous claims. characterized in that

an external influence on the regulatory network is represented by an input node of the equivalent neuronal network.

4. Method in accordance with one of the previous claims. characterized in that

on adaptation of the equivalent neuronal network to the specific gene expression patterns, the preferred networks are those which feature a lower level of networking.

5. Arrangement for identification of pharmaceutical targets

with means for determining a plurality of gene expression patterns of a cell, with the expression rate of the gene of the cell being determined in each case, in which case the means are embodied such that the chronological sequence of the gene expression pattern of the cell can be at least partly reconstructed;

with means for forming a dynamic model of the regulatory network of genome and proteome of the cell by forming an equivalent neuronal network in the following manner:

i) a gene of the genome as well as its associated protein is represented by a neuron (20) of the equivalent neuronal network;

ii) the expression rate of a gene is represented by a non-negative activity of the equivalent neuron (20);

iii) the regulatory effect of a protein on the gene is represented by its synaptic connection (26) from the neuron

equivalent to the protein to the neuron equivalent to the gene;

iv) the type or a regulatory effect (strengthening or inhibiting) is represented in the neuronal network by the leading sign and the strength of the associated synaptic weight (w);

with means for comparing the equivalent neuronal network with the gene expression patterns determined;

with means for adapting the equivalent neuronal network to the gene expression patterns determined; and

with means for deducing the regulatory network of the investigated cells from the adapted neuronal network.